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*wt*  
Sub D10

15. (Amended) The sequence-specific polynucleotide of claim 14, wherein the 3' end of the primer aligns with a highlighted nucleotide position designated as any of the SEQ ID NOS: 1-10.

Sub D11

16. (Amended) The sequence-specific polynucleotide of claim 11 that is between 10 and 50 bases long.

REMARKS

Claims 1-20 are pending in the present application. Claims 1-16 are under examination in the present application. In the Response to Restriction Requirement accompanying this Preliminary Amendment, Applicants elected to prosecute Group I, Claims 1-16, without traverse. In this Preliminary Amendment Applicants select SEQ ID NOS: 1-10 for examination. Marked up claims filed under 37 CFR § 1.121(c)(1)(iii) accompany this preliminary amendment.

In view of the foregoing, Applicants believe all claims now pending in this Application are in condition for allowance. The issuance of a formal Notice of Allowance at an early date is respectfully requested.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at (650) 326-2400.

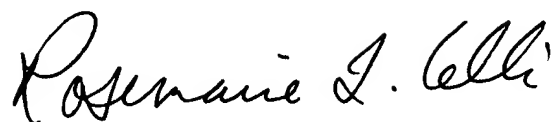
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Respectfully submitted,

A handwritten signature in cursive script, reading "Rosemarie L. Celli".

Rosemarie L. Celli  
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On Nov. 7, 2000

TOWNSEND and TOWNSEND and CREW LLP

By: Rosemarie S. Celli

PATENT  
Attorney Docket No.: 018547-018570US  
Client Reference No.: 8006.7

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Gingeras et al.

Application No.: 09/285,306

Filed: April 2, 2000

For: MYCOBACTERIAL *rpoB*  
SEQUENCES

Examiner: J. Siew

Art Unit: 1656

MARKED UP CLAIMS FILED UNDER 37  
CFR § 1.121(c)(1)(iii) IN ACCOMPANIMENT  
TO PRELIMINARY AMENDMENT

Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

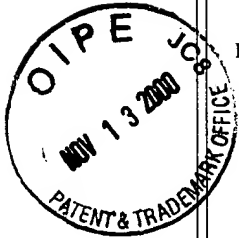
The following marked up version of each claim under examination shows all the changes relative to the previous version of the claim.

1. (Amended) A nucleic acid comprising at least 50 contiguous bases from an *rpoB* sequence designated as any of the SEQ ID NOS: 1-10. [1-181.]

2. (Amended) The nucleic acid of claim 1 comprising a complete *rpoB* sequence designated as any of the SEQ ID NOS: 1-10. [1-181.]

3. (Amended) A set of probes perfectly complementary to and spanning a full-length sequence designated as of the SEQ ID NOS: 1-10. [1-181.]

4. (Amended) A method of classifying a mycobacteria, comprising



providing a sample comprising a mycobacterial rpoB target nucleic acid from a mycobacteria;

determining the sequence of a segment of at least 50 contiguous bases from the target nucleic acid;

comparing the determined sequence to at least one sequence designated as SEQ ID NOS: 1-10; [1-181];

classifying the mycobacteria from the extent of similarity of the compared sequences.

5. (Amended) The method of claim 4, wherein at least 100 contiguous bases are determined from the target nucleic acid.

6. (Amended) The method of claim 4, wherein the determined sequence is compared with at least ten sequences designated as SEQ ID NOS: 1-10 1-181.

7. (Amended) A method of classifying a mycobacteria, comprising providing a sample comprising a mycobacterial rpoB target nucleic acid; and determining the identity of one or more bases in the target sequence at one or more positions corresponding to one or more of the highlighted positions in a sequence designated as any of the SEQ ID NOS: 1-10, [1-181,] the identity of the one or more bases characterizing the species of mycobacteria that is present in the sample.

8. (Amended) The method of claim 7, wherein the identity of at least 10 bases in the target nucleic acid at positions corresponding to highlighted positions in a sequence designated as any of the SEQ ID NOS: 1-10 [1-181] is determined.

9. (Amended) The method of claim 8, wherein the identity of at least 20 bases in the target sequence at highlighted positions designated as any of the SEQ ID NOS: 1-10 [1-181] are identified.

10. (Amended) The method of claim 9, further comprising comparing the 20 determined bases with 20 bases occupying corresponding positions in each of at least ten sequences designated as any of the SEQ ID NOS: 1-10. [1-181.]

11. (Amended) A sequence-specific polynucleotide probe or primer that hybridizes to a segment of a mycobacterial rpoB sequence designated as any of the SEQ ID NOS: 1-10 [1-181] or its complement without hybridizing to the M. tuberculosis sequence designated [ATCC9-Mtb] SEQ ID NO: 1 or its complement, wherein the segment includes a highlighted nucleotide position designated as any of the SEQ ID NOS: 1-10. [1-181.]

12. (Amended) The sequence-specific polynucleotide of claim 11 [9] that is a probe.

13. (Amended) The sequence-specific polynucleotide of claim 12, wherein a central position of the probe aligns with a highlighted nucleotide position designated as any of the SEQ ID NOS: 1-10. [1-181.]

14. (Amended) The sequence-specific polynucleotide of claim 11 [9] that is a primer.

15. (Amended) The sequence-specific polynucleotide of claim 14, wherein the 3' end of the primer aligns with a highlighted nucleotide position designated as any of the SEQ ID NOS: 1-10. [1-181.]

16. (Amended) The sequence-specific polynucleotide of claim 11 [8] that is between 10 and 50 bases long.

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Respectfully submitted,



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